

CRF Errors Corrected by the STIC Systems Branch

Page NO: 1800 RMD
RECEIVED
 4/29/2003
 MAY 05 2003
 (STIC staff)

Serial Number: 09/932, 8/2 A

CRF Processing Date: 4/29/2003
 Edited by: A
 Verified by: A

ENTERED

TECH CENTER 1600/2900

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was wrapped down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Sequence 23 - moved explanation of sequence from
<2137 line to <2237 line

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

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1600

RAW SEQUENCE LISTING

DATE: 04/29/2003

PATENT APPLICATION: US/09/932,812A

TIME: 12:59:30

Input Set : N:\AMC\I932812a.raw

Output Set : N:\CRF4\04292003\I932812A.raw

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1 <110> APPLICANT: Sun, Lee-Hwei K
2     Sun, Bill N
3     Sun, Cecily R
4 <120> TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with
5     increased biological
6     activities
7 <130> FILE REFERENCE: 02SUN2001
C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/932,812A
9 <141> CURRENT FILING DATE: 2001-08-17
10 <160> NUMBER OF SEQ ID NOS: 28
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 29
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
17 <220> FEATURE:
18 <223> OTHER INFORMATION: PCR primer
19 <400> SEQUENCE: 1
20     cccaagcttg gcgcggagat gggggtgca                29
22 <210> SEQ ID NO: 2
23 <211> LENGTH: 27
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: PCR primer
28 <400> SEQUENCE: 2
29     cggatccgtc ccctgtcctg caggcct                27
31 <210> SEQ ID NO: 3
32 <211> LENGTH: 20
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: PCR primer
37 <400> SEQUENCE: 3
38     gagcgcaaatt gttgtgtcga                20
40 <210> SEQ ID NO: 4
41 <211> LENGTH: 28
42 <212> TYPE: DNA
43 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: PCR primer
46 <400> SEQUENCE: 4
47     ggaattctca ttaccgga gacagga                28

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RAW SEQUENCE LISTING

DATE: 04/29/2003

PATENT APPLICATION: US/09/932,812A

TIME: 12:59:30

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49 <210> SEQ ID NO: 5
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51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial Sequence
53 <220> FEATURE:
54 <223> OTHER INFORMATION: PCR primer
55 <400> SEQUENCE: 5
56      tggttttctc gatggaggct gggaggcct      29
58 <210> SEQ ID NO: 6
59 <211> LENGTH: 29
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
62 <220> FEATURE:
63 <223> OTHER INFORMATION: PCR primer
64 <400> SEQUENCE: 6
65      aggcctccca gcctccatcg agaaaacca      29
67 <210> SEQ ID NO: 7
68 <211> LENGTH: 69
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: PCR primer
73 <400> SEQUENCE: 7
74      cggatccggt ggcggttccg gtggaggcgg aagcggcggt ggaggatcag agcgcaaatg      60
75      ttgtgtcga      69
77 <210> SEQ ID NO: 8
78 <211> LENGTH: 21
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: PCR primer
83 <400> SEQUENCE: 8
84      gagtccaaat atggtccccc a      21
86 <210> SEQ ID NO: 9
87 <211> LENGTH: 28
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: PCR primer
92 <400> SEQUENCE: 9
93      ggaattctca ttaccacaga gacagggga      28
95 <210> SEQ ID NO: 10
96 <211> LENGTH: 21
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: PCR primer
101 <400> SEQUENCE: 10
102      cctgagttcg cggggggacc a      21

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TIME: 12:59:30

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104 <210> SEQ ID NO: 11
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106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: PCR primer
110 <400> SEQUENCE: 11
111      gagtccaaat atggtccccc atgccaccca tgcccagcac ctgagttcgc ggggggacca      60
113 <210> SEQ ID NO: 12
114 <211> LENGTH: 70
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: PCR primer
119 <400> SEQUENCE: 12
120      cggatccggt ggcggttccg gtggaggcgg aagcggcggt ggaggatcag agtccaaata      60
121      tgggtcccca      70
123 <210> SEQ ID NO: 13
124 <211> LENGTH: 21
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: PCR primer
129 <400> SEQUENCE: 13
130      gacaaaactc acacatgccc a      21
132 <210> SEQ ID NO: 14
133 <211> LENGTH: 23
134 <212> TYPE: DNA
135 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <223> OTHER INFORMATION: PCR primer
138 <400> SEQUENCE: 14
139      acctgaagtc gcggggggac cgt      23
141 <210> SEQ ID NO: 15
142 <211> LENGTH: 55
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: PCR primer
147 <400> SEQUENCE: 15
148      gacaaaactc acacatgccc accgtgccca gcacctgaag tcgcgggggg accgt      55
150 <210> SEQ ID NO: 16
151 <211> LENGTH: 70
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: PCR primer
156 <400> SEQUENCE: 16
157      cggatccggt ggcggttccg gtggaggcgg aagcggcggt ggaggatcag acaaaaactca      60

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158      cacatgccca                                     70
160 <210> SEQ ID NO: 17
161 <211> LENGTH: 1332
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: HuEPO-L-vFc gamma2 (Figure 2A)
166 <400> SEQUENCE: 17
167      aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc      60
168      ctgctgtcgc tccctctggg cctcccagtc ctgggcgccc caccacgcct catctgtgac      120
169      agccgagtcg tggagaggta cctcttggag gccaaaggag ccgagaatat cagcaggggc      180
170      tgtgtgtaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc      240
171      tatgcctgga agaggatgga ggtcggggcag caggccgtag aagtctggca gggcctggcc      300
172      ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg      360
173      gagcccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg      420
174      cttcgggctc tgggagccca gaaggaagcc atctcccctc cagatgcggc ctcagctgct      480
175      ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc      540
176      ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt      600
177      ggcggttccg gtggaggcgg aagcggcggt ggaggatcag agcgcaaagt ttgtgtcgag      660
178      tgcccaccgt gccagcacc acctgtggca ggaccgtcag tcttctcttt cccccaaaaa      720
179      cccaaggaca ccctcatgat ctcccgacc cctgaggtca cgtgcgtggt ggtggacgtg      780
180      agccacgaag accccgaggt ccagttcaac tggtagctgg acggcgtgga ggtgcataat      840
181      gccaaagaaa agccacggga ggagcagttc aacagcacgt tccgtgtggt cagcgtcctc      900
182      accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa      960
183      ggccctccag cctccatcga gaaaaccatc tccaaaacca aagggcagcc ccgagaacca      1020
184      caggtgtaca ccctgcccc atcccgggag gagatgacca agaaccaggt cagcctgacc      1080
185      tgctgtgtca aaggcttcta ccccgagcgc atcgccgtgg agtgggagag caatgggcag      1140
186      ccggagaaca actacaagac cacacctccc atgctggact ccgacggctc cttcttcttc      1200
187      tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgtctt ctcatgtctc      1260
188      gtgatgcatg aggtctctga caaccactac acgcagaaga gcctctccct gtctccgggt      1320
189      aaatgagaat tc                                     1332
191 <210> SEQ ID NO: 18
192 <211> LENGTH: 436
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide
197      (Figure 2
198      A)
199 <400> SEQUENCE: 18
200      Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Ser Leu
201      1              5              10              15
202      Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
203      20              25              30
204      Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
205      35              40              45
206      Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
207      50              55              60
208      Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg

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Input Set : N:\AMC\I932812a.raw

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209      65              70              75              80
210 Met Glu Val Gly Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
211      85              90              95
212 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
213      100             105             110
214 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
215      115             120             125
216 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
217      130             135             140
218 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
219      145             150             155             160
220 Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
221      165             170             175
222 Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
223      180             185             190
224 Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
225      195             200             205
226 Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
227      210             215             220
228 Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
229      225             230             235             240
230 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
231      245             250             255
232 His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
233      260             265             270
234 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
235      275             280             285
236 Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
237      290             295             300
238 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser
239      305             310             315             320
240 Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
241      325             330             335
242 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
243      340             345             350
244 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
245      355             360             365
246 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
247      370             375             380
248 Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
249      385             390             395             400
250 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
251      405             410             415
252 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
253      420             425             430
254 Ser Pro Gly Lys
255      435
257 <210> SEQ ID NO: 19
258 <211> LENGTH: 1335

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/932,812A

DATE: 04/29/2003
TIME: 12:59:31

Input Set : N:\AMC\I932812a.raw
Output Set: N:\CRF4\04292003\I932812A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:18; Line(s) 196
Seq#:20; Line(s) 293
Seq#:22; Line(s) 390

VERIFICATION SUMMARY

DATE: 04/29/2003

PATENT APPLICATION: US/09/932,812A

TIME: 12:59:31

Input Set : N:\AMC\I932812a.raw

Output Set: N:\CRF4\04292003\I932812A.raw

L:8 M:270 C: Current Application Number differs, Wrong Format